

/organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_lib="NIH_MGC_59"
 /tissue_type="mucoepidermoid carcinoma"
 /lab_host="DH10B (T1 phage-resistant)"
 /note="Organ: lung; Vector: PDNR-LIB (Clontech); Site:1; SfiI (ggccgctggcc); Site:2: SfiI (ggccattatggcc); Double-stranded cDNA was prepared from cell line RNA. 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGGCATTATGGCC-3' and 3' adaptor sequence: 5'-ATTCTAGAGCGCGCGGCAGCATG-dT(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.65 kb (range 0.9-4.0 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH-MGC library."

BASE COUNT 217 a 169 c 246 g 227 t
 ORIGIN

Query Match 90.9%; Score 508.2; DB 12; Length 859;
 Best Local Similarity 98.8%; Pred. No. 7.4e-140;
 Matches 554; Conservative 0; Mismatches 3; Indels 4; Gaps 4;

QY 1 CCGCAATGGCAGCGCAGCCCGGACCTTGTGTAGACAGCCCATGTATGTCTCA 60
 DB 20 CCGCAATGGCAGCGCAGCCCGGACCTTGTGTAGACAGCCCATGTATGTCTCA 79
 QY 61 TGGAGTTTGTGTAGAGACAGCCAGTCCAGTCTTATTGAGGATCCCGCATG 120
 DB 80 TGGAGTTTGTGTAGAGACAGCCAGTCCAGTCTTATTGAGGATCCCGCATG 139
 QY 121 TGTTCACCTGCAAGATGCGGATGAGTGTGTACAAATGAGTTCATGCCA 180
 DB 140 TGTTCACCTGCAAGATGCGGATGAGTGTGTACAAATGAGTTCATGCCA 197
 QY 181 AAGTGAATCCAAAGATCCAGATTAAGGCTCTCCCGCTTATTCTGTTTGTGA 240
 DB 198 AAGTGAATCCAAAGATCCAGATTAAGGCTCTCTCCCGCTTATTCTGTTTGTGA 257
 QY 241 GAAATGGAAGAAAGGTGGCTGGCCGCGCTTACCAAGAGGATATCAAGCAGTGT 300
 DB 258 GAAATGGAAGAAAGGTGGCTGGCCGCGCTTACCAAGAGGATATCAAGCAGTGT 317
 QY 301 GCGTGTCTGTGAGACTTGTATCTGAGAGACTGGGAAGGGATGAGAGATGAGCTGG 360
 DB 318 GCGTGTCTGTGAGACTTGTATCTGAGAGACTGGGAAGGGATGAGAGATGAGCTGG 377
 QY 361 CTCATGTGGAACATTATGACAGCTTTGAAGAAGTACAGCAAGAGACTCCACTG 420
 DB 378 CTCATGTGGAACATTATGACAGCTTTGAAGAAGTACAGCAAGAGACTCCACTG 437
 QY 421 CCATGATGATTTGATGATGATCTGTACAG-TGCTGATGATGCAACAAGTAAATTAATT 479
 DB 438 CCATGATGATTTGATGATGATCTGTACAGTGTGATGATGCAACAAGTAAATTAATT 497
 QY 480 TCTGTGACGC-AAAGCTGGGAAGCAGCTGTGGCTATTTCAGTGTCTTACGAAGCTA 538
 DB 498 TCTGTGACGC-AAAGCTGGGAAGCAGCTGTGGCTATTTCAGTGTCTTACGAAGCTA 557
 QY 539 GCGCTAGGCTTTGTGACGG 559
 DB 558 GCGCTAGGCTTTGTGACGG 578

RESULT 2
 LOCUS AL539434 902 bp mRNA linear EST 16-FEB-2001
 DEFINITION AL539434 LTI_FLO13_FBrn1 Homo sapiens cDNA clone CS0DF033YE07 5
 prime, mRNA sequence.
 ACCESSION AL539434
 VERSION AL539434.1 GI:12868643

KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 902)
 AUTHORS Li, W.-B., Gruber, C., Jesse, J., and Polyes, D.
 TITLE Full-length cDNA libraries and normalization
 JOURNAL Unpublished (2001)
 COMMENT
 Contact: Genoscope
 Genoscope - Centre National de Sequencage
 BP 191 91006 EVRY cedex - France
 Email: sequef@genoscope.cns.fr, Web : www.genoscope.cns.fr.
 Location/Qualifiers

FEATURES
 source
 1..902
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_lib="LTI_FLO13_FBrn1"
 /dev_stage="pooled tissue from post conception fetuses
 week 24 week and 26 week)"
 /lab_host="DH10B"
 /note="Organ: Fetal brain; Vector: PCWSPORT 6; 1st strand
 cDNA was primed with a NotI-oligo(dT) primer. Five prime
 end enriched, double-stranded cDNA was digested with Not I
 and cloned into the Not I and Eco RV sites of the
 PCWSPORT 6 vector. Library was constructed by Life
 Technologies. Contact : Feng Liang Life Technologies, a
 division of Invitrogen 9800 Medical Center Drive Rockville
 , Maryland 20850, USA Fax : (1) 301 610 8371 Email :
 fliang@lifetech.com URL :
 http://fulllength.invitrogen.com"

BASE COUNT 218 a 214 c 265 g 202 t 3 others
 ORIGIN

Query Match 77.9%; Score 435.4; DB 9; Length 902;
 Best Local Similarity 99.8%; Pred. No. 3.2e-118;
 Matches 436; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCGCAATGGCAGCGCAGCCCGGACCTTGTGTAGACAGCCCATGTATGTCTCA 60
 DB 334 CCGCAATGGCAGCGCAGCCCGGACCTTGTGTAGACAGCCCATGTATGTCTCA 393
 QY 61 TGGAGTTTGTGTAGAGACAGCCAGATGTCACAGTCTTATTGAGGATCCCGCATG 120
 DB 394 TGGAGTTTGTGTAGAGACAGCCAGATGTCACAGTCTTATTGAGGATCCCGCATG 453
 QY 121 TGTTCAGCTGCAAGATGCGGATGAGTGTGTACAAATGAGTTCATGCCA 180
 DB 454 TGTTCAGCTGCAAGATGCGGATGAGTGTGTACAAATGAGTTCATGCCA 513
 QY 181 AAGTGAATCCAAAGATCCAGATTAAGGCTCTCCCGCTTATTCTGTTTGTGA 240
 DB 514 AAGTGAATCCAAAGATCCAGATTAAGGCTCTCTCCCGCTTATTCTGTTTGTGA 573
 QY 241 GAAATGGAAGAAAGGTGGCTGGCCGCGCTTACCAAGAGGATATCAAGCAGTGT 300
 DB 574 GAAATGGAAGAAAGGTGGCTGGCCGCGCTTACCAAGAGGATATCAAGCAGTGT 633
 QY 301 GCGTGTCTGTGAGACTTGTATCTGAGAGACTGGGAAGGGATGAGAGATGAGCTGG 360
 DB 634 GCGTGTCTGTGAGACTTGTATCTGAGAGACTGGGAAGGGATGAGAGATGAGCTGG 693
 QY 361 CTCATGTGGAACATTATGACAGCTTTGAAGAAGTACAGCAAGAGACTCCACTG 420
 DB 694 CTCATGTGGAACATTATGACAGCTTTGAAGAAGTACAGCAAGAGACTCCACTG 753
 QY 421 CCATGATGATTTGGAT 437
 DB 754 CCATGATGATTTGGAT 770

RESULT 3

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AF039235      AF039235      1866 bp      mRNA      linear      EST 13-MAR-1998
LOCUS         AF039235      Human (J. Swensen) Homo sapiens cDNA clone 91-13, mRNA
DEFINITION    sequence.
ACCESSION     AF039235
VERSION       AF039235.1 GI:2773139
KEYWORDS      EST.
SOURCE        human.
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE     1 (bases 1 to 1866)
AUTHORS       Mili,Y., Swensen,J., Statluch-Elidens,D., Futreal,P.A., Harshman,K.,
              Tavtigian,S., Liu,Q., Cochran,C., Bennett,L.M. and Ding,W.
              A strong candidate for the breast and ovarian cancer susceptibility
              gene BRCA1
              Science 266 (5182), 66-71 (1994)
JOURNAL       Science 266 (5182), 66-71 (1994)
MEDLINE       95025896
COMMENT       Contact: Jeff Swensen
              Medical Informatics
              University of Utah
              391 Chipeta Way, Suite D-2, Salt Lake City, UT 84108, USA
              Email: jeffsw@epiun5.med.utah.edu
              region between D17S1321 and D17S855.
FEATURES
  Source
    1..1866
    /organism="Homo sapiens"
    /db_xref="taxon:9606"
    /map="17q21"
    /clone="91-13"
    /clone_lib="Human (J. Swensen)"
    /note="Organ: Hip; Vector: pBluescript; Site_1: EcoRI;
    Library constructed by Dr. Marian Young and Dr. Pamela
    Gehron Robey (NIDCR)"
BASE COUNT    466 a      423 c      568 g      408 t      1 others
ORIGIN
Query Match   77.3%; Score 432.2; DB 9; Length 1866;
Best Local Similarity 99.3%; Pred. No. 4e-117;
Matches 434; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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RESULT 4
LOCUS         AL520188      935 bp      mRNA      linear      EST 13-FEB-2001
DEFINITION    AL520188 LTI_NFL004_NBC2 Homo sapiens cDNA clone CS0DB005YN06 5
prime, mRNA sequence.
ACCESSION     AL520188
VERSION       AL520188.1 GI:12783681
KEYWORDS      EST.
SOURCE        human.
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE     1 (bases 1 to 935)
AUTHORS       Li,W.B., Gruber,C., Jesse,J. and Polayes,D.
              Full-length cDNA libraries and normalization
              Unpublished (2001)
JOURNAL       Unpublished (2001)
COMMENT       Contact: Genoscope
              Genoscope - Centre National de Sequencage
              BP 191 91006 Evry cedex - France
              Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
FEATURES
  Source
    1..935
    /organism="Homo sapiens"
    /db_xref="taxon:9606"
    /clone="CS0DB005YN06"
    /clone_lib="LTI_NFL004_NBC2"
    /sex="male"
    /tissue_type="neuroblastoma cells"
    /lab_host="DH10B"
    /note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA
    was primed with a NotI-oligo(dT) primer. Five prime end
    enriched, double-stranded cDNA was digested with Not I and
    cloned into the Not I and Eco RV sites of the pCMVSPORT 6
    vector. Library was normalized. Library was constructed
    by Life Technologies. Contact : Feng Liang Life
    Technologies, a division of Invitrogen 9800 Medical Center
    Drive Rockville, Maryland 20850, USA Fax : (1) 301 610
    8371 Email : fliang@lifetech.com URL :
    http://fulllength.invitrogen.com"
BASE COUNT    231 a      206 c      287 g      208 t      3 others
ORIGIN
Query Match   76.3%; Score 426.4; DB 9; Length 935;
Best Local Similarity 99.8%; Pred. No. 1.6e-115;
Matches 427; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db 361 AACATATGACGAGCTTTTGAAGAAGTGCACACACAGAGACCTCCACCTGCATGATG 420
 QY 430 ATTGGAT 437
 |||||
 Db 421 ATTGGAT 428

RESULT 5
 AM245514
 LOCUS 577 bp mRNA linear EST 07-JAN-2000
 DEFINITION 2823004.sp1rme NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2823004 5',
 mRNA sequence.
 ACCESSION AM245514
 VERSION AM245514.1 GI:6588507
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 577)
 NIH-MGC http://mgi.nci.nih.gov/
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Other ESTs: 2823004.3prime
 Contact: Robert Strausberg, Ph.D.
 Email: rgapbs-remail.nih.gov
 Tissue Procurement: DCTD/DPF CDNA Library Preparation: Ling
 Hong/Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E.
 Consortium (LINP) DNA Sequencing by: Berkeley MGC sequencing
 project clone distribution: MGC clone distribution information can
 be found through the I.M.A.G.E. Consortium/LINP at:
 www.bio.lnlnl.gov/dbtrp/image/image.html Base Calling / Quality
 Scores: PHRED from University of Washington Genome Center. Vector
 Priming: cross-match from University of Washington Genome Center
 PHRAP suite. Poly-T identification: patchmatch.pl from Berkeley
 Drosophila genome project. University of Washington Genome Center:
 http://www.genome.washington.edu
 plate: LHCMI0 row: 0 column: 5
 High quality sequence stop: 487.
 Location/Qualifiers
 1..577
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone IMAGE:2823004"
 /clone_11b="NIH_MGC_7"
 /tissue_type="small cell carcinoma"
 /cell_line="MGC3"
 /lab_host="DH10B (phage-resistant)"
 /note="Organ: lung; Vector: pOTB7; Site_1: XhoI; Site_2:
 EcoRI; cDNA made by oligo-dT priming. Directionally
 cloned into EcoRI/XhoI sites using the following 5'
 adaptor: GGCACGAC(G). Size-selected >500bp for average
 insert size 1.8kb. Library constructed by Ling Hong in
 the laboratory of Gerald M. Rubin (University of
 California, Berkeley) using ZAP-cDNA synthesis kit
 (Stratagene) and Superscript II RT (Life Technologies)."
 BASE COUNT 129 a 133 c 179 g 136 t
 ORIGIN
 Query Match 76.1%; Score 425.2; DB 10; Length 577;
 Best Local Similarity 99.3%; Pred. No. 2.8e-115;
 Matches 427; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 8 GGCACGGACGACGCCGCGACCTTGATGATGACGACGCCCATGATGTTTCATGAGTT 67
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 Db 103 GGGAAAGGACGACGCCGCGACCTTGATGATGACGACGCCCATGATGTTTCATGAGTT 162
 |||||
 QY 68 TTGTGTTGAGGACGACGACGATGTCACGTTGATGATGATGATGATGATGATGATG 127
 |||||
 Db 163 TTGTGTTGAGGACGACGACGATGTCACGTTGATGATGATGATGATGATGATGATG 222
 |||||
 QY 128 CTGCAGAGATGCCGATGAGTGGAGTGTGACATGATGATGATGATGATGATGATGATG 187
 |||||

Db 223 CTGCAGAGATGCCGATGAGTGGAGTGTGATGATGATGATGATGATGATGATGATG 282
 QY 188 CTCGAGGACCTCCGAGTAAGCGCTCTCCGCTCTATGATGATGATGATGATGATG 247
 |||||
 Db 283 CTCGAGGACCTCCGAGTAAGCGCTCTCTCCGCTCTATGATGATGATGATGATGATG 342
 |||||
 QY 248 GAGGAAAGGTGCGCTGCGCGCGCTTACCAAGAGAGATATCAAGCAGTGTGCGTGTG 307
 |||||
 Db 343 GAGGAAAGGTGCGCTGCGCGCGCTTACCAAGAGAGATATCAAGCAGTGTGCGTGTG 402
 |||||
 QY 308 TGTGACCTTTGATTAACCTGAGAGACTGGGAGAGGAGATGAAGATGAGAGCTGATGT 367
 |||||
 Db 403 TGTGACCTTTGATTAACCTGAGAGACTGGGAGAGGAGATGAAGATGAGAGCTGATGT 462
 |||||
 QY 368 GGAACATATGAGAGCTTTTGAAGAAGTGCACACAGAGACCTCCACCTGCATGGA 427
 |||||
 Db 463 GGAACATATGAGAGCTTTTGAAGAAGTGCACACAGAGACCTCCACCTGCATGGA 522
 |||||

QY 428 TGATTTGGAT 437
 |||||
 Db 523 TGATTTGGAT 532

RESULT 6
 AL527833
 LOCUS 934 bp mRNA linear EST 13-FEB-2001
 DEFINITION AL527833.LTI_NFL003.NBC3 Homo sapiens cDNA clone CSODC027YD22 5
 prime, mRNA sequence.
 ACCESSION AL527833
 VERSION AL527833.1 GI:12791326
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 934)
 Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
 TITLE Full-length cDNA libraries and normalization
 JOURNAL Unpublished (2001)
 COMMENT Contact: Genoscope
 Genoscope - Centre National de Sequencage
 BP 191 91006 Evry cedex - France
 Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
 Location/Qualifiers
 1..934
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="CSODC027YD22"
 /clone_11b="LTI_NFL003_NBC3"
 /sex="male"
 /tissue_type="neuroblastoma cells"
 /lab_host="DH10B"
 /note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA
 was primed with a NotI-oligo(dT) primer. Five prime end
 enriched, double-stranded cDNA was digested with Not I and
 cloned into the Not I and Eco RV sites of the pCMVSPORT 6
 vector. Library was normalized. Library was constructed
 by Life Technologies. Contact : Feng Liang Life
 Technologies, a division of Invitrogen 9800 Medical Center
 Drive Rockville, Maryland 20850, USA Fax : (1) 301 610
 8371 Email : fliang@lifestech.com URL :
 http://fulllength.invitrogen.com" 1 others
 BASE COUNT 230 a 209 c 289 g 205 t
 ORIGIN
 Query Match 76.1%; Score 425.2; DB 9; Length 934;
 Best Local Similarity 99.3%; Pred. No. 3.5e-115;
 Matches 427; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 8 GGCACGGACGACGCCGCGACCTTGATGATGACGACGCCCATGATGTTTCATGAGTT 67
 |||
 Db 52 GGGAAAGGACGACGCCGCGACCTTGATGATGACGACGCCCATGATGTTTCATGAGTT 111
 |||||

```

OY 68 TTGTGTGAGGACGACCGATGTCACCTGCTTATTGAGATACCCGATTTGTTGAC 127
    |||||||
Db 112 TTGTGTGAGGACGACCGATGTCACCTGCTTATTGAGATACCCGATTTGTTGAC 171
    |||||||
OY 128 CTCGAAGATGCGGATGAGTGTGATGATGATGATGATGATGATGATGATGATGAT 187
    |||||||
Db 172 CTCGAAGATGCGGATGAGTGTGATGATGATGATGATGATGATGATGATGATGAT 231
    |||||||
OY 188 CTCGAAGATGCGGATGAGTGTGATGATGATGATGATGATGATGATGATGATGAT 247
    |||||||
Db 232 CTCGAAGATGCGGATGAGTGTGATGATGATGATGATGATGATGATGATGATGAT 291
    |||||||
OY 248 GAAAGAAAGTGGCTGGCGCGGCTTACCAAGAGATATCAAGCCATGTCCTGTC 307
    |||||||
Db 292 GAAAGAAAGTGGCTGGCGCGGCTTACCAAGAGATATCAAGCCATGTCCTGTC 351
    |||||||
OY 308 TGTGACTTTGATGATGAGAGAGTGGAGAGGATGAGATGAGATGAGATGAGATGAG 367
    |||||||
Db 352 TGTGACTTTGATGATGAGAGAGTGGAGAGGATGAGATGAGATGAGATGAGATGAG 411
    |||||||
OY 368 GGAACATTTATGACAGCTTTTGAAGAAGTACACACCAAGAGATGATGATGATGAT 427
    |||||||
Db 412 GGAACATTTATGACAGCTTTTGAAGAAGTACACACCAAGAGATGATGATGATGAT 471
    |||||||
OY 428 TGTATTGAT 437
    |||||||
Db 472 TGTATTGAT 481
    |||||||

RESULT 7
LOCUS BF776383 481 bp mRNA linear EST 25-APR-2001
DEFINITION B271175 MARC 3BOV Bos taurus cDNA 5' mRNA sequence.
ACCESSION BF776383
VERSION BF776383.1 GI:12124283
KEYWORDS EST.
SOURCE cov.
ORGANISM Bos taurus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
            Bovidae; Bovinae; Bos.
REFERENCE 1 (bases 1 to 481)
AUTHORS Smith,T.P.L., Grosse,W.M., Freking,B.A., Roberts,A.J., Stone,R.T.,
        Casas,E., Wray,J.E., White,J., Cho,J., Fahrenkrug,S.C., Bennett,
        G.L., Heaton,M.P., Laegreid,W.W., Rohrer,G.A., Chitko-McKown,C.G.,
        Perlea,G., Holt,I., Karamycheva,S., Ilang,F., Quackenbush,J. and
        Keele,J.W.
        Sequence evaluation of four pooled-tissue normalized bovine cDNA
        libraries and construction of a gene index for cattle
        Genome Res. 11 (4), 626-630 (2001)
COMMENT Contact: Smith TPL
        USDA, ARS, US Meat Animal Research Center
        PO Box 166, Clay Center, NE 68933-0166, USA
        Tel: 402 762 4366
        Fax: 402 762 4390
        Email: smith@email.marc.usda.gov
        Single pass sequencing. Bases called and alt trimmed with phred
        v0.980904.e. Vector identified by cross_match with the -minscore 18
        and -minmatch 12 options.
PCR PRIMERs
FORWARD: AGGAACAGCTATGACCAT
BACKWARD: GTTTCACAGTCACGACG
Plate: 90 row: F column: 22
Seq primer: ATTAGTGACACTATAG.

FEATURES
            source
                location/Qualifiers
                    1..481
                        /organism="Bos taurus"
                        /db_xref="taxon:9913"
                        /clone_lib="MARC 3BOV"
                        /tissue_type="pooled"
                        /lab_host="DH10B"
                        /note="Vector: PCMV SPORT6; Site_1: NotI; Site_2: SalI;

BASE COUNT 125 a 98 c 146 g 112 t
ORIGIN
Query Match 73.2%; Score 409; DB 12; Length 481;
Best Local Similarity 92.1%; Pred. No. 1,7e-110;
Matches 443; Conservative 0; Mismatches 35; Indels 3; Gaps 1.
OY 7 TGGCAGGACGACCGCCGACCTTTGTTGATGACAGAGGCCATGATGTTGATGAGT 66
    |||||||
Db 1 TGGCAGGACGACCGCCGACCGCCGACCTTTGTTGATGACAGAGGCCATGATGAGT 60
    |||||||
OY 67 TTTGTGTTGAGAGACGACCGATGATGATGATGATGATGATGATGATGATGATGATGAT 126
    |||||||
Db 61 TTTGTGTTGAGAGACGACCGATGATGATGATGATGATGATGATGATGATGATGATGAT 120
    |||||||
OY 127 GCTGCAAGATGCGGATGAGTGAAGTGTATCAATGATGATGATGATGATGATGATGAT 186
    |||||||
Db 121 GCTGCAAGATGCGGATGAGTGAAGTGTATCAATGATGATGATGATGATGATGATGAT 180
    |||||||
OY 187 ACTGCAAGAGACTCCAGATTAAGCGCTCTTCCGCTCTATTACTTGTGAGAAAT 246
    |||||||
Db 181 ACTGCAAGAGACTCCAGATTAAGCGCTCTTCCGCTCTATTACTTGTGAGAAAT 240
    |||||||
OY 247 GGAAGAAAGAGTGGCTGGCGCGGCTTACCAAGAGAGATATCAAGCCATGTCCTGT 306
    |||||||
Db 241 GGAAGAAAGAGTGGCTGGCGCGGCTTACCAAGAGAGATATCAAGCCATGTCCTGT 300
    |||||||
OY 307 CTGTGACTTTGATGATGAGAGACTGGAGAGGAGATGAAGATGAGATGAGATGAG 366
    |||||||
Db 301 CTGTGACTTTGATGATGAGAGACTGGAGAGGAGATGAAGATGAGATGAGATGAG 360
    |||||||
OY 367 TGGACATTTATGACAGCTTTTGAAGAAGTACACACCAAGAGATGATGATGATGAT 426
    |||||||
Db 361 TGGACATTTATGACAGCTTTTGAAGAAGTACACACCAAGAGATGATGATGATGAT 420
    |||||||
OY 427 ATGATTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 486
    |||||||
Db 421 ATGATTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 477
    |||||||
OY 487 C 487
Db 478 C 478

RESULT 8
LOCUS B1109957 587 bp mRNA linear EST 26-JUN-01
DEFINITION 602901477F1 NCL_CGAP_Mam5 Mus musculus cDNA clone IMAGE:503125.
ACCESSION B1109957
VERSION B1109957.1 GI:14560858
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
REFERENCE 1 (bases 1 to 587)
AUTHORS NIH-NHG http://mgc.ncl.nih.gov/.
TITLES NATIONAL Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
        Email: cgabs@email.nih.gov
        Tissue Procurement: Lotmar Hennighausen Ph.D., Robin Humphreys
        cDNA Library Preparation: Life Technologies, Inc.
        DNA Sequencing by: Incyte Genomics, Inc.
        Clone distribution: MGC clone distribution information can be
        found through the I.M.A.G.E. Consortium/LNL at:
        http://image.llnl.gov
        Plate: L1AM1087 row: 1 column: 20

```

RESULT	10
BF308215	
LOCUS	
DEFINITION	624 bp mRNA linear EST 21-NOV-2000 60187465P1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4121368 5'
ACCESSION	mRNA sequence. BF308215

VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
BF308215.1	GI:11255396	human.	Homo sapiens	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.	1 (bases 1 to 824)	NIH-MGC http://mgc.nci.nih.gov/ . National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)		Contact: Robert Strausberg, Ph.D. Email: cqapb5-remail.nih.gov Tissue Procurement: ATCC
				cDNA Library Preparation: Ling Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNLN at: image.lnl.nih.gov Plate: LNCMI03 row: a column: 17 High quality sequence stop: 721.				
FEATURES		Location/Qualifiers						
Source		1..824						
		/organism="Homo sapiens"						
		/db_xref="taxon:9606"						
		/clone="IMAGE:4121368"						
		/clone_lib="NIH_MGC_17"						
		/tissue_type="rhabdomyosarcoma"						
		/lab_host="DH10B (phage-resistant)"						
		/note="Organ: muscle; Vector: pOTB7; site_1: EcoRI; site_2: XhoI; cDNA made by oligo-dT priming. directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."						
BASE COUNT		210 a 159 c 262 g 193 t						
ORIGIN								
Query Match		61.3%; Score 342.8; DB 12; Length 824;						
Best Local Similarity		96.5%; Pred. No. 1e-90;						
Matches	361;	Conservative	0;	Mismatches	12;	Indels	1;	Gaps
QY	1	CCGCATATGGCAGCGACGACGCCCGGACCTTGTTGTCAGCAGGCCCATGTATGTGTCA	60					
Db	9	CCGCATATGGCAGCGACGACGCCCGGACCTTGTTGTCAGCAGGCCCATGTATGTGTCA	68					
QY	61	TGGAGTTTGTGTAGGACAGCACCAGATGTCACAGTCTTATTGAGATTCACCGCATG	120					
Db	69	TGGAG-TTGTGTGTAGGACAGCACCAGATGTCACAGTCTTATTGAGATTCACCGCATG	127					
QY	121	TGTTACGCTGCAAGATCCCGATGAGATGGAATTTACAAATAGATTTAGTTCTATGCCA	180					
Db	128	TGTTACGCTGCAAGATCCCGATGAGATGGAATTTAGCAATAGATTTAGTTCTATGCCA	187					
QY	181	AAGTGAATCCAGAGACTCCACAGATTAAGCGCTCTCCCGCTCTATTACTTGTTTGTGA	240					
Db	188	AAGTGAATCCAGAGACTCCACAGATTAAGCGCTCTCCCGCTCTATTACTTGTTTGTGA	247					
QY	241	GAATATGGAAGAAAGATGGCTGCGCGGCTTTCACAGAGAGATATCAAGCCAGTCT	300					
Db	248	GAATATGGAAGAAAGATGGCTGCGCGGCTTTCACAGAGAGATATCAAGCCAGTCT	307					
QY	301	GGCTCTCTGTGACTTTGATCTGAGAGACTGGGAAGGGGATGAAGAGATGAGAGCTGG	360					
Db	308	GGCTCTCTGTGACTTTGATCTGAGAGACTGGGAAGGGGATGAAGAGATGAGAGCTGG	367					
QY	361	CTCATGTGGAACAT 374						
Db	368	ATTGAGGCGAGCAT 381						

LOCUS	635 bp	MRNA	linear	EST 12-JUN-2001
BC975246	635 bp	MRNA	linear	EST 12-JUN-2001
DEFINITION	60284315F1 NCI_CGAP_Mam4 Mus musculus cDNA clone IMAGE:4979028 5'			
ACCESSION	BC975246			
VERSION	BC975246.1			
KEYWORDS	EST.			
SOURCE	house mouse.			
ORGANISM	Mus musculus			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 635)			
AUTHORS	NIH-MGC http://mgc.nci.nih.gov/ .			
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)			
JOURNAL	Unpublished (1999)			
COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgaps-remail.nih.gov Tissue Procurement: Lothar Hennighausen Ph.D., Priscilla Furth Ph.D. cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LMNL) DNA Sequencing by: Incyte Genomics, Inc. cDNA distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LMNL at: http://image.llnl.gov Plate: LHM10976 row: 1 column: 13 High quality sequence stop: 612. Location/Qualifiers 1..635 /organism="Mus musculus" /strain="NMRI" /db_xref="taxon:10090" /clone="IMAGE:4979028" /clone_id="NCI_CGAP Mam4" /tissue_type="tumor, gross tissue" /dev_stage="5 months" /lab_host="DH10B" /note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: SalI; Site_2: NotI; Cloned unidirectionally. Primer: oligo dT. Library constructed by Life Technologies. Investigators providing samples: Lothar Hennighausen/Priscilla Furth. NIH Reference for transgenic model: Li et al., Cell Growth and Differentiation 7,3-11 (1996)."			
FEATURES				
source				
BASE COUNT	148 a 146 c 188 g 153 t			
ORIGIN				
Query Match	56.0% Score 313.2; DB 13; Length 635;			
Best Local Similarity	87.1% Pred. No. 5.6e-82;			
Matches 378; Conservative	0; Mismatches 53; Indels 3; Gaps 3;			
QY	21 GCCCGGACCTGTGTGTAAGACAGCCCATGTATGTGTCATGAGAGTTTGTGTGAGGAC 80			
Db	12 GCCCGGACTGTGTGTAGACAGACCCAAATATGTTTCATGAGAGTTGTGCTTGTAGGAC 71			
QY	81 AGCAGCGATGTCACGTGCTTATTGTAGAGATCACCGCATGTGTTCAGCTGCAGAAATGCC 140			
Db	72 AGCAGCGAGTCAGTGTGCTCATGTAGAGACACCGCGCTGTGTACGCTGCAGGAATGGT 131			
QY	141 GATGAGTGTGAGTTGTACAAATGATGTGATGTATATGCCCAAGTCAACTCCAGGACATCC 200			
Db	132 GATGAGTGTGAGTTGTATTAACGAATTTGATATGTCACCAAGTCAAGGACATCC 191			
QY	201 CAGATTAAGACCTGTGTCCCGCTATATTCCTG-TTTGTGAGAAATGGAAGGAAGAT 259			
Db	192 CAGATTAAGCTTGTGTGCTCCTCATTAATCTGCTCTTGTGAGAAATGGAAGGAAGAT 251			
QY	260 GGCTGTGCGCGC-GCTTACCAAGAGATATCAAGCCAGTGTGCTGTCTGTGACCTTTG 318			
Db	252 GGCTGTGCGCTGTGCTCAACAAGGAGATATAAGCCTGTGTGCTGTCTGTGACCTTGG 311			
QY	319 ATAAGTGGAGAGACTGGGAAAGGAGATGA-AAGATGAGAGCTGTGCTCATGTGGAACATTAT 377			
Db	312 ATAAGTGGAGAGACTGGGAAAGGAGAGACTGAGGTGAGAGCTGTGCTCAGTGAAGACATTAT 371			

[illegible]

oligo-dt primer and directionally cloned using the Lambda
ZAP II Vector Kit by Stratagene"
BASE COUNT 84 a 71 c 96 g 71 t 3 others
ORIGIN

Query Match 48.7%; Score 272.4; DB 14; Length 325;
Best Local Similarity 89.5%; Pred. No. 5.5e-70;
Matches 291; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

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OY 107 GGATCACCAGCATGTGTCAGCTGCAGAAATGCCGATGAGTGTACATGAGAT 166
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1 GGACCACCCGATCGTTTCAGCTGCAGAAATGATGTGTGAGCTGTACAAAGAGAT 60
OY 167 TGAGTTCTATGCCAAGTGAATCCAGAGACTCCAGATAAGCGCTTCCCGCTCTAT 226
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 61 TGANTTCATGCCAANTGAATCCAGAGACTCCAGATAAGCGCTGTGCTGCCAT 120
OY 227 TACTGTGTTTGAGAAAATGAGAGAAAAGTGCGCTGCGCGGCTTACCAAGAGGA 286
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 121 TACTGTGTTTGAGAGAAATGAGAGAAAGTGCGCTGCGCTGCACTCACCAGAGGA 180
OY 287 TATCAGCCAGTGTGCTGTCTGTGACTTTGATTAAGAGAGACTGGAGAGGATGA 346
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 181 TATAAAGCCCGTTGTGCTCTGTGACTTCATTAAGAGAGACTGGAGAGAGATGA 240
OY 347 AGAGATGAGCTGCTCATGTGAACATTATGCAGAGCTTTGAGAGAGTCAACACAA 406
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 241 CGAGATGAGAGCTGGCGCAGAGTGAACACTATTCAGAGCTTTGAGCAAGGTCAAGCACTAA 300
OY 407 GAGACCTCCACCTGCCATGATGAT 431
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 301 GAGACCTCCCGCTGCCATGATGAT 325
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Search completed: March 20, 2003, 03:50:53
Job time : 1823 secs